



## SEQUENCE LISTING

<110> Prayaga, Suhhirdas K  
Shimkets, Richard A  
  
<120> Novel Polypeptides and Polynucleotides Encoding Same  
  
<130> 15966-615  
  
<140> 09/732,436  
<141> 2000-12-07  
  
<150> 60/169,887  
<151> 1999-12-09  
  
<150> 60/170,230  
<151> 1999-12-10  
  
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<170> PatentIn Ver. 2.1

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b7c*  
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<212> DNA  
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cagcctcttt ttacacaagg gctgtctga tgcttggaaat agggccttc tggacaaact 180  
ccagactgga tttcatcagc agctggaaage cctggagacc tgctttggta tagaggatgg 240  
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gggagtagcat ttcttcttga aagagagggaa attcaggaac tgtacctggg aggttgcgt 360  
aatggtaaag ggattttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420  
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<211> 154  
<212> PRT  
<213> Homo sapiens

<400> 2  
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1 5 10 15

Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His  
20 , 25 30

Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser  
35 40 45

Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His  
50 55 60

Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys

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TECH CENTER 1600/2900

65 70 75 80

Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg  
85 90 95

Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn  
100 105 110

Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr  
115 120 125

Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn  
130 135 140

Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu  
145 150

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<213> Homo sapiens

<220>  
<221> misc\_feature  
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nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 180  
nnnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnaa agtcaggtg atttctgccc tccataagat 240  
gcaccagcag atcttcagcc tcttttaca caaggcctg tctgatgctt ggaatagggc 300  
cttcctggas aaactccaga ctggattca tcagcagctg gaagacctgg agacctgctt 360  
tggtagatag gatggaaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420  
aaagaggtac ttccagggag tacatttctt cttgaagag agaaaattca ggaactgtac 480  
ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc acaaaaacttc aagaaaaaga 540  
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<210> 4  
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<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (24)..(68)  
<223> Wherein Xaa is any amino acid.

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Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

20                    25                    30  
 Xaa  
 35                    40                    45  
 Xaa  
 50                    55                    60  
 Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His  
 65                    70                    75                    80  
 Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp  
 85                    90                    95  
 Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu  
 100                  105                  110  
 Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser  
 115                  120                  125  
 Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln  
 130                  135                  140  
 Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp  
 145                  150                  155                  160  
 Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln  
 165                  170                  175  
 Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys  
 180                  185                  190  
 Val Ile Tyr Leu Ala Glu Glu  
 195


 <210> 5  
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 <212> DNA  
 <213> Homo sapiens

<400> 5  
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 gcagccgagc tgccgtctggc agacaacttc atgcctcccg tgccgcgcgg cgacctggcc 240  
 aacatgacag gcctgctgca tctgagcctg tcgcggaaaca ccattccgcga cgtggctgcc 300  
 ggcgccttcg cgcacctgca ggcctgcgt gccctgcacc tggatggcaa cgggctgacc 360  
 tcactggcgc agggccagct ggcggcctg gtcaacttgc gtcacctcat cctcagcaac 420  
 aaccagctgg cagcgtctggc ggcggcgcctg ctggatgatt gtggcgagac actggaggac 480  
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 cccgaccacat ttttctcccg cctggccctg ctgcgcaggc cccggggctc gcccgcctct 720  
 gcccgtgtgc tggcctttgg cggaaacccc ctgcactgca actgcgcgcgtt ggtgtggctg 780  
 cgtgcgttgg cgcgggagga cgacctcgag gcctgcgcgt ccccacctgc tctggcggc 840  
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cgctcaccac ctctggctgt gcccgcaggt cggccggctg ccctgcgctg ccgggcagtg 960  
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agccgtcccc ggcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080  
ggtggcatct tcacctgcat tgccgccaat gcagctggcg aggccacagc tgctgtggag 1140  
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cgggacgggg atccctgatgc tctcaccctca ccctccgctg cctctgcttc tgccaaagg 1260  
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gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgtta ccagatccag 1380  
tacaacagct cggctgatga catcctcgta tacaggatga tcccggcgga gagccgctcg 1440  
ttcctgctga cggacctggc gtcaaggccgg acctacgatc tgtgcgtgtc cgccgtgtat 1500  
gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgccccttctccacc 1560  
gaacctgcgc tgccgccatg cggggcgccg cacgctccct tcctggcgac cacgatgatc 1620  
atcgcgctgg gcgggtcat cgtagcctcg gtactggctt tcatcttcgt gctgctaatt 1680  
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<210> 6  
<211> 628  
<212> PRT  
<213> Homo sapiens

<400> 6  
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Ser Ser Pro Pro Gln Ser Ala Thr Pro Ser Pro Cys Pro Arg Arg Cys  
20 25 30  
  
Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala  
35 40 45  
  
Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu  
50 55 60  
  
Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala  
65 70 75 80  
  
Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg  
85 90 95  
  
His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu  
100 105 110  
  
His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg  
115 120 125  
  
Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala  
130 135 140  
  
Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp  
145 150 155 160  
  
Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu  
165 170 175

Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu  
180 185 190

Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg  
195 200 205

Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu  
210 215 220

Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser  
225 230 235 240

Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu  
245 250 255

Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys  
260 265 270

Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu  
275 280 285

Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro  
290 295 300

Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val  
305 310 315 320

Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu  
325 330 335

Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu  
340 345 350

Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala  
355 360 365

Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly  
370 375 380

Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro  
385 390 395 400

Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Pro Ser Ala Ala Ser Ala  
405 410 415

Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln  
420 425 430

Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln  
435 440 445

Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser  
450 455 460

Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser  
465 470 475 480

Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val  
485 490 495

Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro  
500 505 510

Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly  
515 520 525

Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly  
530 535 540

Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met  
545 550 555 560

Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro  
565 570 575

Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro  
580 585 590

Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala  
595 600 605

His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu  
610 615 620

Pro Val Gly Pro  
625

*full DS UNIT*

<210> 7  
<211> 802  
<212> DNA  
<213> Equus caballus

<400> 7  
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ttttccccat ggcctcctg ccctctctct tgacgc<sup>c</sup>cct ggtggtgtac gagttatggc 180  
cctgtggagc tctgggctgt gacctgcctc agaacc<sup>a</sup>cat cctggtagc aggaagaact 240  
tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaaag 300  
acttcaggtt ccccccaggac atggcggatg gcaggcagtt cccagaggcc caggccgcgt 360  
ctgtcctcca cgagatgctc cagcagatct tcagccctcg ccacacagag cgctcgctg 420  
ctgcctggaa cacgaccctc ctggacgaac tctgcacggg actccttcgg cagctggaaag 480  
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gccctacact ggccgtgaag aggtacttcc gggggatcca tctctacctg aaagagaaga 600  
aatacagtga ctgtgcctgg gagattgtcc gaatggaaat catgagatcc ttctcttcat 660  
cagcaaacct gcaaggaagg ttaagaatga aggatggaga cctgggctca ccttggaaatg 720  
attctcccta actactgggt catgttaccc ttgcataatgt ccttggtcat ttcaaaaaggc 780  
tcttatttct gcttttgtct ag 802

<210> 8  
<211> 195  
<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr  
1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
195

<210> 9

<211> 195

<212> PRT

<213> Equus caballus

<400> 9

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser  
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu  
20 25 30

Arg Lys Gln Glu Thr Leu Arg Val Leu His Gln Met Glu Thr Ile Ser  
35 40 45

Pro Pro Ser Cys Leu Lys His Arg Thr Asp Phe Arg Phe Pro Gln Glu  
50 55 60

Gln Leu Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu  
65 70 75 80

Gln Glu Met Leu Gln Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Arg Leu Leu Ala Gly Leu  
100 105 110

His Gln Gln Leu Glu Asp Leu Asn Thr Cys Leu Asp Glu Gln Thr Gly  
115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Gly Pro Thr Leu Ala Val Lys  
130 135 140

Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu Thr Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Val Asp Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp Leu  
180 185 190

Gly Ser Pro  
195

<210> 10  
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<212> PRT  
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<220>  
<223> Description of Artificial Sequence:pfam00143  
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Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn  
20 25 30

Thr Thr Leu Leu Glu Glu Phe Cys Thr Glu Leu Asp Arg Gln Leu Thr  
35 40 45

Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu Ala Pro  
50 55 60

Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr  
65 70 75 80

Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys  
85 90 95

Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser  
100 105 110

Ser Thr Ala Leu Gln  
115

<210> 11  
<211> 194  
<212> PRT  
<213> Felis catus

<400> 11  
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys  
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu  
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro  
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp  
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val  
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser  
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly  
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val  
115 120 125

Glu Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp  
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu  
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met  
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser  
180 185 190

Glu Lys

<210> 12

<211> 195  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr  
1 5 10 15

Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu  
20 25 30

Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser  
35 40 45

Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu  
50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser  
85 90 95

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu  
100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly  
115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys  
130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser  
165 170 175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu  
180 185 190

Ser Ser Pro  
195

*but D  
and*

<210> 13  
<211> 195  
<212> PRT  
<213> Equus caballus

<400> 13

Met Ala Leu Leu Pro Ser Leu Leu Thr Ala Leu Val Val Tyr Glu Leu  
1 5 10 15

Trp Pro Cys Gly Ala Leu Gly Cys Asp Leu Pro Gln Asn His Ile Leu  
20 25 30

Val Ser Arg Lys Asn Phe Val Leu Leu Gly Gln Met Ser Arg Ile Ser  
 35 40 45

Ser Ala Ile Cys Leu Lys Asp Arg Lys Asp Phe Arg Phe Pro Gln Asp  
 50 55 60

Met Ala Asp Gly Arg Gln Phe Pro Glu Ala Gln Ala Ala Ser Val Leu  
 65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
 85 90 95

Ser Ala Ala Trp Asn Thr Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu  
 100 105 110

Leu Arg Gln Leu Glu Asp Leu Asp Thr Cys Leu Glu Gln Glu Met Gly  
 115 120 125

Glu Glu Glu Ser Ala Leu Gly Thr Val Arg Pro Thr Leu Ala Val Lys  
 130 135 140

Arg Tyr Phe Arg Gly Ile His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser  
 145 150 155 160

Asp Cys Ala Trp Glu Ile Val Arg Met Glu Ile Met Arg Ser Phe Ser  
 165 170 175

Ser Ser Ala Asn Leu Gln Gly Arg Leu Arg Met Lys Asp Gly Asp Leu  
 180 185 190

Gly Ser Pro  
 195

*but*  
*D5*  
*Um*

<210> 14  
 <211> 195  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr  
 1 5 10 15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
 20 25 30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
 35 40 45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
 50 55 60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
 65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser  
 85 90 95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
100 105 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
115 120 125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
130 135 140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
145 150 155 160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
165 170 175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
180 185 190

Gly Ser Ser  
195

<210> 15  
<211> 65  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Consensus  
sequence

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Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser  
1 5 10 15

Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln  
20 25 30

Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys  
35 40 45

Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu  
50 55 60

Gln  
65

<210> 16  
<211> 166  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
1 5 10 15

Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu  
20 25 30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln  
35 40 45

Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln  
50 55 60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
65 70 75 80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
85 90 95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
100 105 110

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
115 120 125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
130 135 140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu  
145 150 155 160

Thr Gly Tyr Leu Arg Asn  
165

<210> 17  
<211> 165  
<212> PRT  
<213> Homo sapiens

*but D5 cent*

<400> 17  
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn

100                    105                    110  
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
 115                    120                    125  
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
 130                    135                    140  
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145                    150                    155                    160  
 Leu Arg Ser Lys Glu  
 165  
 <210> 18  
 <211> 189  
 <212> PRT  
 <213> Mus musculus  
 <400> 18  
 Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr  
 1                    5                            10                    15  
 Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu  
 20                    25                            30  
 Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser  
 35                    40                            45  
 Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu  
 50                    55                            60  
 Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu  
 65                    70                            75                    80  
 Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser  
 85                    90                            95  
 Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu  
 100                    105                            110  
 His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly  
 115                    120                            125  
 Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg  
 130                    135                            140  
 Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser  
 145                    150                            155                    160  
 Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser  
 165                    170                            175  
 Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys  
 180                    185

<210> 19  
<211> 195  
<212> PRT  
<213> Antilocapra americana

<400> 19  
Met Ala Gln Leu Leu Pro Leu Leu Thr Ala Leu Val Leu Cys Ser Tyr  
1 5 10 15

Gly Pro Val Gly Ser Leu Gly Cys Asp Leu Pro His Asn Ser Ala Pro  
20 25 30

Leu Ser Arg Lys Thr Leu Val Leu Leu Asp Gln Met Arg Arg Val Ser  
35 40 45

Pro Val Leu Cys Leu Lys Asp Arg Arg Asp Phe Gln Phe Pro Arg Glu  
50 55 60

Val Val Asn Gly Ser Gln Phe Gln Lys Asn Gln Thr Val Ser Val Leu  
65 70 75 80

His Glu Met Leu Gln Gln Ile Phe Asn Leu Leu His Thr Ala Arg Ser  
85 90 95

Ser Ala Ala Trp Asn Asn Thr Leu Leu Glu Glu Leu His Thr Ala Leu  
100 105 110

His Gln Gln Leu Gln Gly Leu Glu Thr Cys Leu Val Gln Ala Met Gly  
115 120 125

Glu Glu Asp Ser Val Leu Thr Ala Asp Ser Pro Met Leu Met Leu Lys  
130 135 140

Arg Tyr Phe Gln Arg Ile Arg Leu Tyr Leu Asp Glu Lys Lys His Ser  
145 150 155 160

Gly Cys Ala Trp Glu Leu Val Arg Met Glu Ile Arg Arg Ala Phe Ser  
165 170 175

Ser Thr Ala Asp Leu Gln Glu Ser Leu Arg Ser Lys Asp Gly Asp Leu  
180 185 190

Ala Ser Ser  
195

*but  
D  
and*

<210> 20  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus sequence

<400> 20

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala  
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile  
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val  
35 40

<210> 21  
<211> 184  
<212> PRT  
<213> Equus caballus

<400> 21  
Met Ala Leu Pro Val Ser Leu Leu Met Ala Leu Val Val Leu Ser Cys  
1 5 10 15

His Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro His Thr His Ser Leu  
20 25 30

Gly Asn Thr Arg Val Leu Met Leu Leu Gly Gln Met Arg Arg Ile Ser  
35 40 45

Pro Phe Ser Cys Leu Lys Asp Arg Asn Asp Phe Gly Phe Pro Gln Glu  
50 55 60

Val Phe Asp Gly Asn Gln Phe Arg Lys Pro Gln Ala Ile Ser Ala Val  
65 70 75 80

His Glu Thr Ile Gln Gln Ile Phe His Leu Phe Ser Thr Asp Gly Ser  
85 90 95

Ser Ala Ala Trp Asp Glu Ser Leu Leu Asp Lys Leu Tyr Thr Gly Leu  
100 105 110

Tyr Gln Gln Leu Thr Glu Leu Glu Ala Cys Leu Ser Gln Glu Val Gly  
115 120 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Leu Leu Ala Val Arg  
130 135 140

Arg Tyr Phe Gln Arg Ile Ala Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Phe Ser  
165 170 175

Ser Ser Thr Asn Leu Pro Gln Ser  
180

<210> 22  
<211> 92  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> Description of Artificial Sequence:Consensus  
sequence

<400> 22  
Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu  
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys  
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp  
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly  
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala  
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln  
85 90

<210> 23  
<211> 3144  
<212> DNA  
<213> Homo sapiens

<400> 23

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tcttcgatcc ggaaaatctt accggcatcc tccttagggag ggattattat tattatttt 180  
ctttaatctg gaagagaaga gaacaagttg tgctttccc cccttcttct tgctaaacgc 240  
catggatata actgaataag cggctcaggg attccccgc gtggacgtcc gaggccacca 300  
tctgcctgca ttccggag ccggcggagg gtttagctcg agtctgtctc gggcgggaa 360  
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gccggggta gatgctgcct cgcccaggcg ctgagtgacc agaccatgga gaccctgctt 480  
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gcaagcggct ttggattgtctatg 3144

<210> 24  
<211> 832  
<212> PRT  
<213> Homo sapiens

<400> 24

Leu Glu Ser Val Ser Gly Gly Glu Gly Cys Val Ala Glu Pro Gly Ser  
1 5 10 15

Pro Gly Ala Pro Arg Ser Arg Pro Arg Cys His Pro Ala Gly Gly Arg  
20 25 30

Cys Cys Leu Ala Gln Ala Leu Ser Asp Gln Thr Met Glu Thr Leu Leu  
35 40 45

Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys  
50 55 60

Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu  
65 70 75 80

Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg  
85 90 95

Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg  
100 105 110

Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg

115                    120                    125

Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser  
130                    135                    140

Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu  
145                    150                    155                    160

Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn  
165                    170                    175

Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu Leu  
180                    185                    190

Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu Pro  
195                    200                    205

Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu Asp  
210                    215                    220

His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu Gln  
225                    230                    235                    240

Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu Pro  
245                    250                    255

Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala Thr  
260                    265                    270

Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu His  
275                    280                    285

Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp Asp  
290                    295                    300

Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe Trp  
305                    310                    315                    320

His Val Arg Glu Glu Phe Val Cys Glu Pro Pro Leu Ile Thr Gln  
325                    330                    335

His Thr His Lys Leu Leu Val Leu Glu Gly Gln Ala Ala Thr Leu Lys  
340                    345                    350

Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile His Trp Val Ala Pro  
355                    360                    365

Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr Ala Val Tyr Asp Asn  
370                    375                    380

Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln Asp Ser Gly Ala Phe  
385                    390                    395                    400

Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala Thr Ala Met Val Glu  
405                    410                    415

Val Ser Ile Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr

420                    425                    430

Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr  
435                    440                    445

Ser Arg Gly Gly Gly Ser Gly Gly Glu Pro Pro Lys Ser Pro  
450                    455                    460

Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr Thr Ser Ala Leu  
465                    470                    475                    480

Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln  
485                    490                    495

Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile  
500                    505                    510

Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr  
515                    520                    525

Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr  
530                    535                    540

Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala  
545                    550                    555                    560

Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr  
565                    570                    575

Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala Thr Leu Leu Val Phe  
580                    585                    590

Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro  
595                    600                    605

Ser Lys Met Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly  
610                    615                    620

Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln  
625                    630                    635                    640

Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala  
645                    650                    655

Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser Ser Leu Gly Ser  
660                    665                    670

Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser  
675                    680                    685

Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala  
690                    695                    700

Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg  
705                    710                    715                    720

Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser

725                    730                    735

Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu  
740                    745                    750

Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp  
755                    760                    765

Met Gly Asp Phe Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly  
770                    775                    780

Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu  
785                    790                    795                    800

Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly  
805                    810                    815

Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val  
820                    825                    830

<210> 25  
<211> 98  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:IFAbd Domain  
13-110

<400> 25  
Gln Phe Gln Lys Glu Asp Ala Ala Ile Thr Ile Tyr Glu Met Leu Gln  
1                    5                    10                    15

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn  
20                    25                    30

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn  
35                    40                    45

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr  
50                    55                    60

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg  
65                    70                    75                    80

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr  
85                    90                    95

Ile Val

<210> 26

<211> 183  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:pfam00143  
Domain 5-187

<400> 26  
Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys Asn Ser Val Cys  
1 5 10 15

Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg  
20 25 30

Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys  
35 40 45

Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly  
50 55 60

Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn  
65 70 75 80

Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala  
85 90 95

Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln  
100 105 110

Leu Thr Arg Leu Glu Ala Cys Val Leu Gln Glu Val Glu Glu Gly Glu  
115 120 125

Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg  
130 135 140

Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser  
145 150 155 160

Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr  
165 170 175

Tyr Ser Ser Thr Ala Leu Gln  
180

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D  
W  
C  
Cont